

09/357709

Docket 242/026
Express Mail
EL199138787US

10/11/01

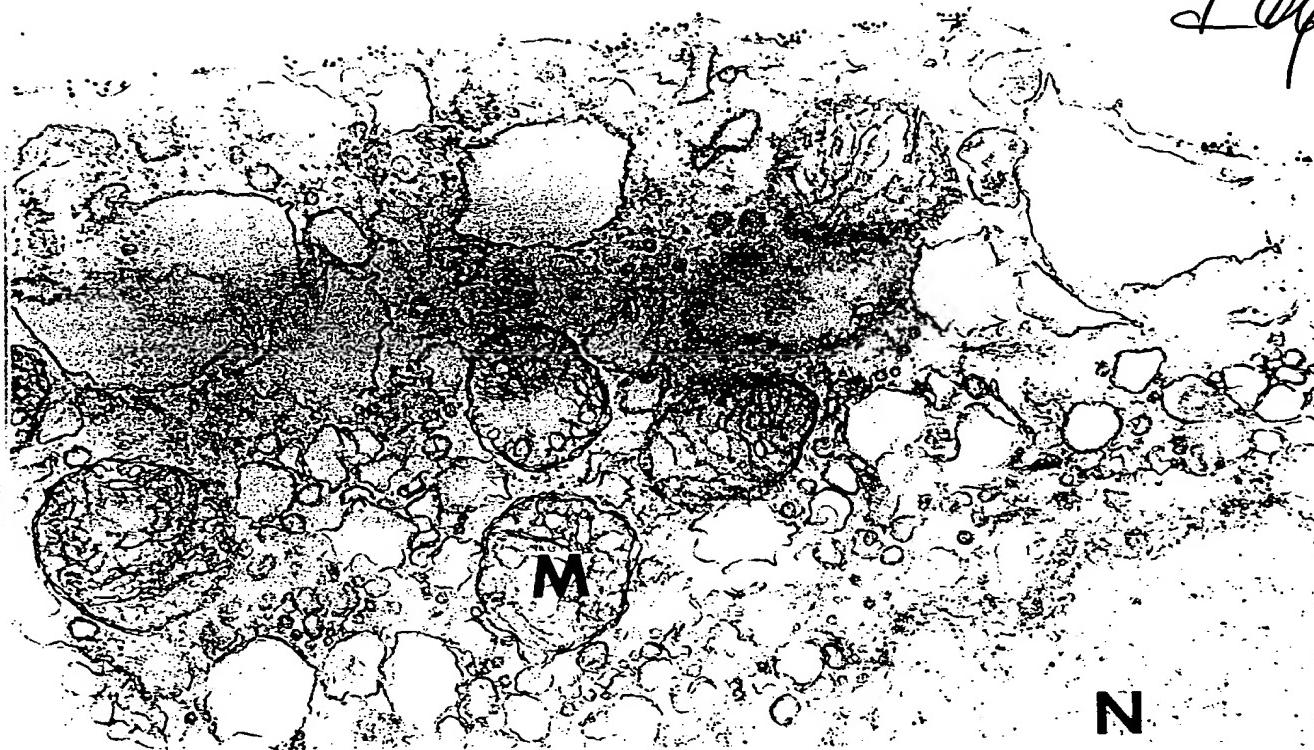


FIGURE 1

**Docket 242/026
Express Mail
EL199138787US**

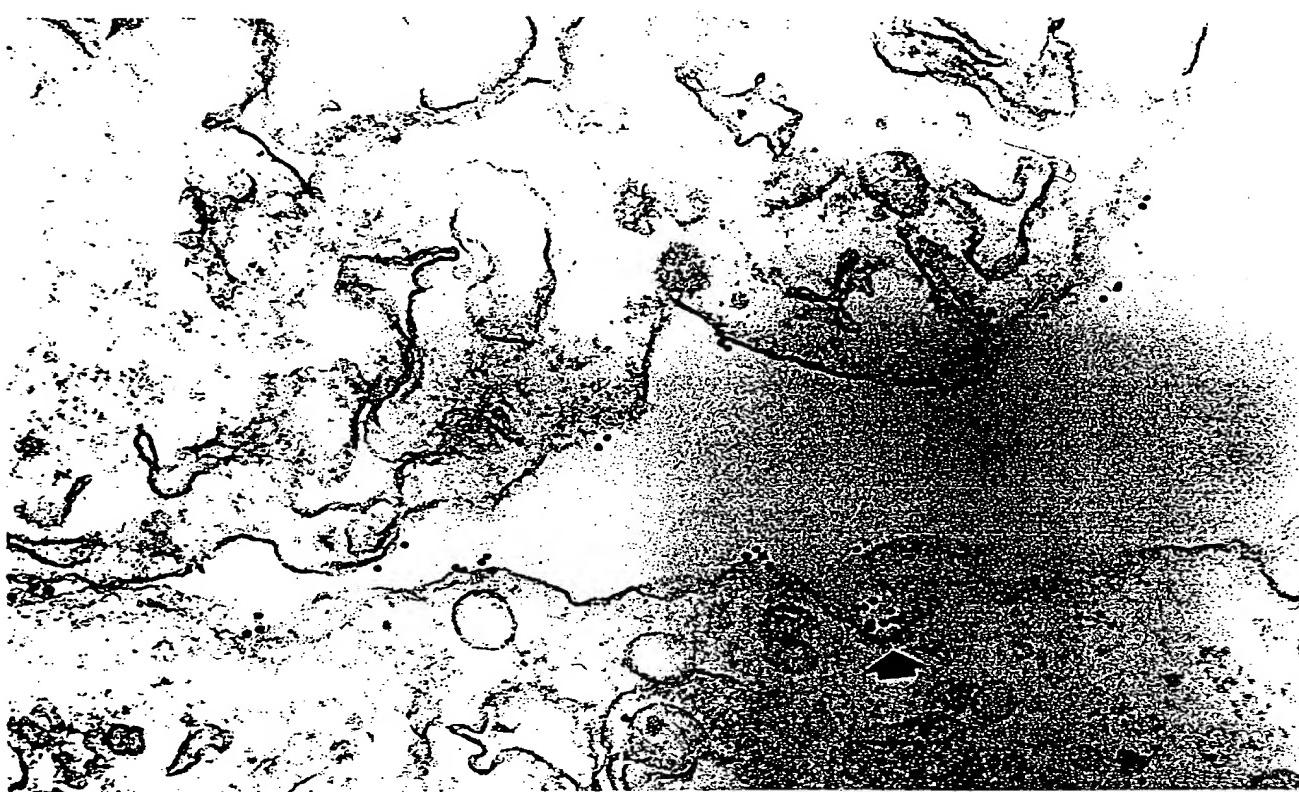


FIGURE 2

Docket 242/026
Express Mail
EL199138787US



FIGURE 3

Docket 242/026
Express Mail
EL199138787US



FIGURE 4

Docket 242/026
Express Mail
EL199138787US

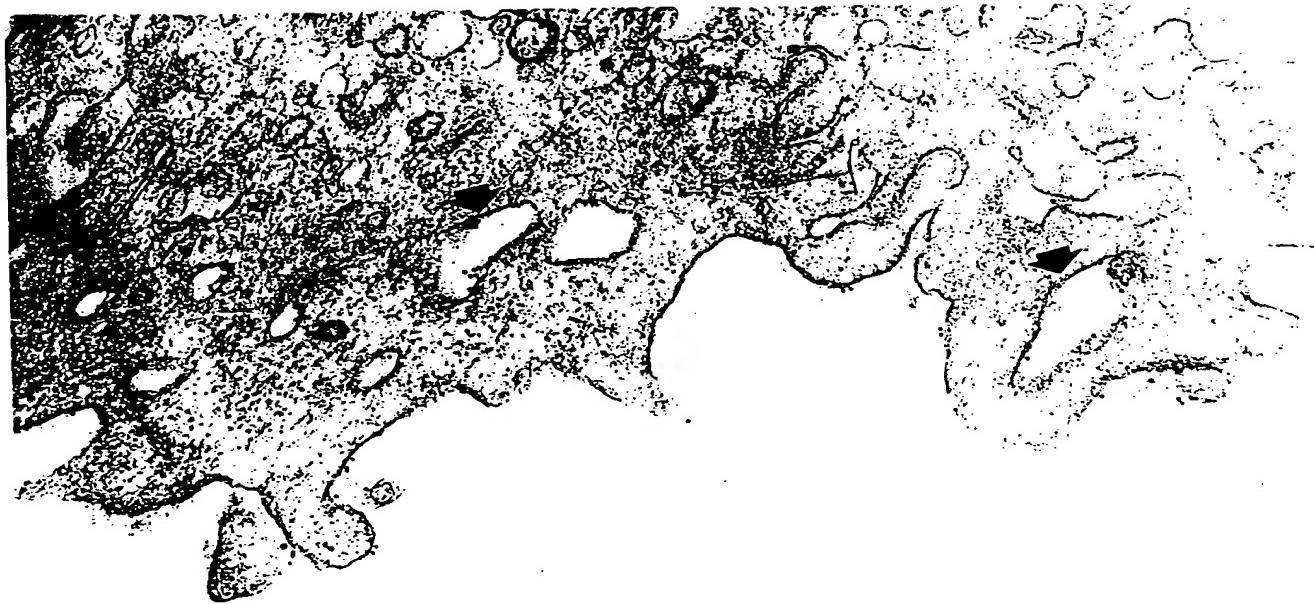


FIGURE 5

Docket 242/026
Express Mail
EL199138787US

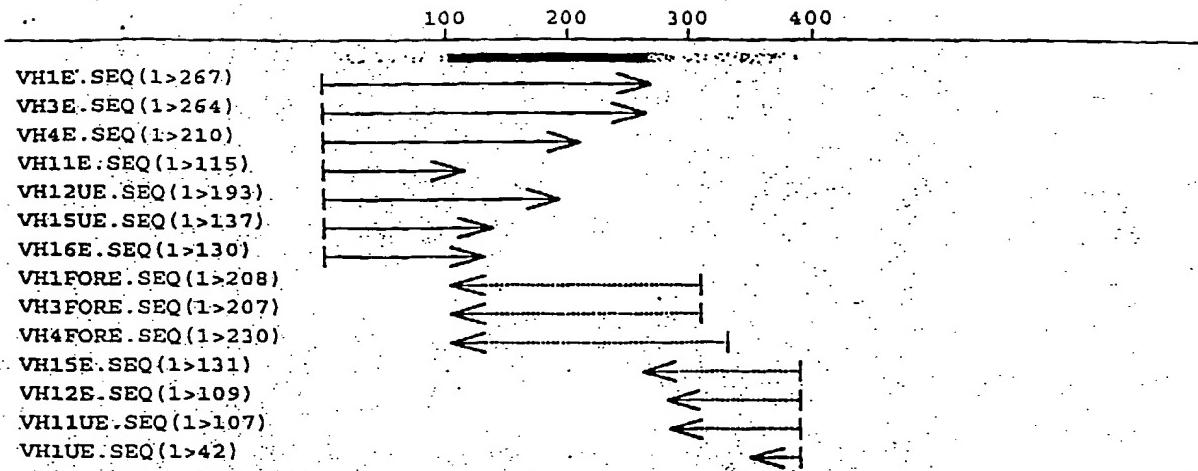


FIGURE 6

Enzymes : All 74 enzymes (No Filter)
Settings: Linear, Certain Sites Only, Standard Genetic Code

	Dde I	Ava II	Alu I	Ava II	Eco57 I	
	Pst I	Sau96 I	Pvu II	Sau96 I	Bsr I	
SEQ. ID. NO. 1	TCTCCTGTCAGGAAC TG CAGGTGCTCTCTGAGGTCCAGCTGCAACAGTCTGGACCTGAACTGGTGAAG					70
SEQ. ID. NO. 2	AGAGGACACTCTTGACGTCCACAGGAGAGACTCCAGGTGACGTTGTCAGACCTGGACTTGACCACTTC					
SEQ. ID. NO. 3	<u>S P V R N C R C P L . G P A A T V W T . T G E</u>					
SEQ. ID. NO. 4	<u>L L S G T A G V L S E V O L O Q O S G P E L V K</u>					
SEQ. ID. NO. 5	<u>L S C O E L Q V S S L R S S C N S L O L N W . S</u>					
	Hph I	Bsp6 II	EcoRV			Dra III
SEQ. ID. NO. 1	CCTGGGACTTCAGTGAGGATATCTGCAAGACTCTGGATAACATTCACTGAATATACCATACTGGG					140
SEQ. ID. NO. 2	GGACCTGAA GT CACT CCT ATAGGAC GT T CTGAAGACCTATGTGTAAGT GACTTATATGGTATGTGACCC					
SEQ. ID. NO. 3	<u>A W D F S E D I L Q D F W I H I H . I Y H I T L G</u>					
SEQ. ID. NO. 4	<u>P G T S V R I S C K T S G Y T F T E Y T J H W</u>					
SEQ. ID. NO. 5	<u>L G L O . G Y P A R L L D T H S L N I P Y T G</u>					
	Hph I	Nco I				Rsa I
SEQ. ID. NO. 1	TGAAGCAGAGCCATGGAAAGAGCCTTGAGTGATTGAAACATCAATCTAACATGGGGTACCCACTA					210
SEQ. ID. NO. 2	ACTTCGTCTCGTACCTTCTCGAACACTAACCTTTGTAGTTAGGATTGTTACCAACATGGTGGAT					
SEQ. ID. NO. 3	<u>E A E P W K E P . V O W K H O S . Q W W Y H L</u>					
SEQ. ID. NO. 4	<u>V K Q S H G K S L E W I G N I N P N N G G T T Y</u>					
SEQ. ID. NO. 5	<u>S R A M E R A L S G L E T S I L T M V V P P</u>					
	Taq I	Hae III	Acc I	Bsr I	Rsa I	Alu I
SEQ. ID. NO. 1	CAATCAGAAGTTGAGGACAAGGCCACATTGACTTAGACAAGTCTCCAGTACAGGGTACATGGAGCTC					280
SEQ. ID. NO. 2	GTTAGCTTCAAGCTCTGTTCCGGTGTAACTGACATCTGTTCAAGGAGGTATGTCGGATGTACCTCGAG					
SEQ. ID. NO. 3	<u>O S E V R G O G H I D C R O V L Q Y S L H G A</u>					
SEQ. ID. NO. 4	<u>N O K F E D K A T L T V D K S S S T A Y M E L</u>					
SEQ. ID. NO. 5	<u>T I R S S R T R P H . L I T S P P V O P T . W S S</u>					
	Dde I	Hinf I	Pst I	Alu I	Bsr I	Sau96 I
SEQ. ID. NO. 1	CGCACGCTAACATCTGAGGATTCTGAGTCTATTATGTGAGCTGGTTGGAACTTGTGACTA GTGGGCC					350
SEQ. ID. NO. 2	GCGTCGGATTGTAGACTCTAACAGCTCAGATAATAACAGTCGACCAACCTTGAAACTGATGACCCCGG					
SEQ. ID. NO. 3	<u>P O P N I . G F C S L L L C S W L E L . L L G P</u>					
SEQ. ID. NO. 4	<u>R S L T S E D S A V Y Y C A A G W N F D Y W G</u>					
SEQ. ID. NO. 5	<u>A A . H L R I L O S I I V O L V . G T L T T G A</u>					
	Dde I	Alw26 I				Hae III
SEQ. ID. NO. 1	AAGGCACCACTCTCACAGTCTCTCAGCCAAAACGACACCC					391
SEQ. ID. NO. 2	TTCCGTGGTGAGAGTGTAGAGGAGTCGGTTTGCTGTGGG					
SEQ. ID. NO. 3	<u>R H H S H S L L S O N O T</u>					
SEQ. ID. NO. 4	<u>O G T T L T V S S A K T T P</u>					
SEQ. ID. NO. 5	<u>K A P L S O S P O P K R H P</u>					

FIGURE 7

Docket 242/026
Express Mail
EL199138787US

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>115)	Seq2(1>125)	Similarity	Gap Number	Gap Length	Consensus Length
J591VH.PRO	MUVHIIA.PRO	Index			
(1>115)	(1>125)	75.6	2	10	125

+10	+20	+30	+40	+50
EVQLQQSGPELVKPGTSVRISCKTSGYTFTEYTI	-HWVKOSHGKSLEWIGNINPNNGGT			
EVQLQQSGPELVKPG:SV:ISCK:SGYTF:Y	: :WVKQS.GKSLEWIG:INP.NGGT:			
EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNNWVKOSPGKSLEWIGDINPGNGGTS				
+10	+20	+30	+40	+50
+60	+70	+80	+90	+100
YNQKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAAG-----	WNFDYWQGQTT			+110
YNQKF:KATLTVDKSSSTAYM:L.SLTSEDSAVYYCA G	...FDYWQGQTT			
YNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGTT				
+70	+80	+90	+100	+110
LTVSS				+120
:TVSS				
VTVSS				

FIGURE 8

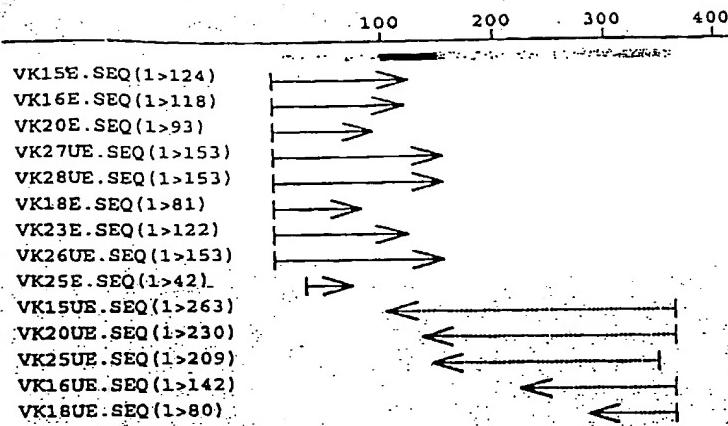


FIGURE 9

Enzymes: All 74 enzymes (No Filter)
Settings: Linear, Certain Sites Only, Standard Genetic Code

Alu I Hph I

SEQ. ID. NO. 9 TTATGGAGCTGATGGAACATTGAATGCCAATCTCCAAATCCATGTCCATGTCACTAGGGAGAGA + 70
SEQ. ID. NO. 10 AATATACTCGACTACCCCTTGTAACATTACTGGGTTAGAGGGTTAGGTACAGGTACAGTCATCCTCT

SEQ. ID. NO. 11 L Y G A D G N I V M T Q S P K S M S M S V G E
SEQ. ID. NO. 12 Y M E L M G T L P N L P N P C P C O . E R
SEQ. ID. NO. 13 I W S . W E H C N D P I S O I H V H V S R R E

Hae III Bsr I

SEQ. ID. NO. 9 GGGTACCTTGACTCTGCAAGGCCAGTGAGAATGTGGTTACTTATGTTCTGGTATCACAGAAACAGA + 140
SEQ. ID. NO. 10 CCCAGTGGAACTGGACGTTGGGTCACTCTAACCCAATGAATACAAAGGACCATAGTTGTCTTGGTCT

SEQ. ID. NO. 11 R V T L T C K A S E N V V T Y V S W Y O O K P E
SEQ. ID. NO. 12 G S P . P A R P V R H W L L H F P G I N R N O
SEQ. ID. NO. 13 G H L D L O G O . E C G Y L C F L V S T E T R

A1w26 I Fok I Hpa II Rsa I Ava II Bsr I Sau96 I Dpn I BsaO I Pvu I Mbo I

SEQ. ID. NO. 9 GCAGTCTCTAACTGCTGATATACTGGGGCATCCAACCGGTACACTGGGTCCCCGATCCCTCACAGGC + 210
SEQ. ID. NO. 10 CGTCAGAGGATTGACGACTATATGCCCGTAGGTTGGCATGTGACCCCAGGGCTAGCGAAGTGTCCG

SEQ. ID. NO. 11 O S P K L L I Y G A S N R Y T G V P D R F T G
SEQ. ID. NO. 12 S S L L N C . Y T G H P - T G T L G S P I A S O A
SEQ. ID. NO. 13 A V S . T A D I R G I O P V H W G P R S L H R

Mbo I Dpn I Bsp6 II Mbo II Eco57 I

SEQ. ID. NO. 9 AGTGGATCTGCAACAGATTCACTCTGACCATCAGCAGTGTGCAGGCTGAAGACCTTGCAGATTACT + 280
SEQ. ID. NO. 10 TCACCTAGACGTTGCTAAAGTGAGACTGGTAGTCGTACACGTCGACTTCTGAAACGTCTAATAGTGA

SEQ. ID. NO. 11 S G S A T O F T L T I S S V O A E D L A D Y H
SEQ. ID. NO. 12 V D L O O I S L . P S A V C R L K T L O I I T
SEQ. ID. NO. 13 O W I C N R F H S . D H O O C A G . R P C R L S L

Au I Rsa I Ava II Sau96 I Alu I

SEQ. ID. NO. 9 GTGGACAGGGTTACAGCTATCCGTACACGTTGGAGGGGGACCAAGCTGGAAATAAACGGGCTGATGC + 350
SEQ. ID. NO. 10 CACCTGTCCCAATGTCGATAGGCATGTGCAAGCCTCCCCCTGGTTCGACCTTATTTGCCGACTACG

SEQ. ID. NO. 11 C G Q G Y S Y P Y T F G G G T K L E I K R A D A
SEQ. ID. NO. 12 V D R V T A : R T R S E G G P S W K . N G L M
SEQ. ID. NO. 13 W T G L O L S V H V R R G . D O A G N K T G . C

SEQ. ID. NO. 9 TGACCAACTGTA
SEQ. ID. NO. 10 → 363
ACGTGGTTGACAT

SEQ. ID. NO. 11 A P T V
SEQ. ID. NO. 12 L H O L Y
SEQ. ID. NO. 13 C T N C →

FIGURE 10

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>107) J591VK.PRO	Seq2(1>111) MUVKV.PRO	Similarity Index	Gap Number	Gap Length	Consensus Length
(1>107)	(1>109)	60.4	2	2	109

^10	^20	^30	^40	^50
NIVMTQSPKSMMSMSVGERVTLTCKAS-ENVVTTYVSWYQQKPEQSPKLLIYGASNRYTGVP				
: I MTQSP .S: S :S: G: RVT: TC: AS :	.. Y: :WYQQKP.	S PKLLIY AS:	..:GVP	
DIOMTQSPSSLSASLGDRVITTCRASQDDISNYLNWYQQKPGGSPKLLIYYASRLHSGVP				
^60	^70	^80	^90	^100
DRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSY-PYTFGGGTKEIK				
.RF:GSGS:TD: :LTIS: : :ED:A.Y C QG: : P	TFGGGTKEIK			
SRFSGSGSGTDYSLTTISNLEQEDIATYFCQQQGNTLPPRTFGGGTKLEIK				
^70	^80	^90	^100	

FIGURE 11